

SEQUENCE LISTING

<110> Degussa AG

<120> A process for producing L-amino acids using strains of the Enterobacteriaceae family

<130> 020481 BT

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 32

<212> DNA

<213> Synthetic sequence

<220>

<221> Primer

<222> (1)..(32)

<223> galP1

<400> 1

cacaatctag ataaaccata ttggagggca tc

32

<210> 2

<211> 25

<212> DNA

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<222> (1)..(25)

<223> galP2

<400> 2

gggaggaagc ttggggagat taatc

25

<210> 3

<211> 1446

<212> DNA

<213> Escherichia coli

<220>

<221> DNA fragment

<222> (1)..(1446)

<223> PCR product

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<221> CDS

<222> (33)..(1427)
 <223> galP coding region

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	1 5	
ggg cgg tca aac aag gca atg acg ttt ttc gtc tgc ttc ctt gcc gct	101	
Gly Arg Ser Asn Lys Ala Met Thr Phe Phe Val Cys Phe Leu Ala Ala		
10 15 20		
ctg gcg gga tta ctc ttt ggc ctg gat atc ggt gta att gct ggc gca	149	
Leu Ala Gly Leu Leu Phe Gly Leu Asp Ile Gly Val Ile Ala Gly Ala		
25 30 35		
ctg ccg ttt att gca gat gaa ttc cag att act tcg cac acg caa gaa	197	
Leu Pro Phe Ile Ala Asp Glu Phe Gln Ile Thr Ser His Thr Gln Glu		
40 45 50 55		
tgg gtc gta agc tcc atg atg ttc ggt gcg gca gtc ggt gcg gtg ggc	245	
Trp Val Val Ser Ser Met Met Phe Gly Ala Ala Val Gly Ala Val Gly		
60 65 70		
agc ggc tgg ctc tcc ttt aaa ctc ggg cgc aaa aag agc ctg atg atc	293	
Ser Gly Trp Leu Ser Phe Lys Leu Gly Arg Lys Ser Leu Met Ile		
75 80 85		
ggc gca att ttg ttt gtt gcc ggt tcg ctg ttc tct gcg gct gcg cca	341	
Gly Ala Ile Leu Phe Val Ala Gly Ser Leu Phe Ser Ala Ala Ala Pro		
90 95 100		
aac gtt gaa gta ctg att ctt tcc cgc gtt cta ctg ggg ctg gcg gtg	389	
Asn Val Glu Val Leu Ile Leu Ser Arg Val Leu Leu Gly Leu Ala Val		
105 110 115		
ggt gtg gcc tct tat acc gca ccg ctg tac ctc tct gaa att gcg ccg	437	
Gly Val Ala Ser Tyr Thr Ala Pro Leu Tyr Leu Ser Glu Ile Ala Pro		
120 125 130 135		
gaa aaa att cgt ggc agt atg atc tcg atg tat cag ttg atg atc act	485	
Glu Lys Ile Arg Gly Ser Met Ile Ser Met Tyr Gln Leu Met Ile Thr		
140 145 150		
atc ggg atc ctc ggt gct tat ctt tct gat acc gcc ttc agc tac acc	533	
Ile Gly Ile Leu Gly Ala Tyr Leu Ser Asp Thr Ala Phe Ser Tyr Thr		
155 160 165		
ggt gca tgg cgc tgg atg ctg ggt gtg att atc atc ccg gca att ttg	581	
Gly Ala Trp Arg Trp Met Leu Gly Val Ile Ile Ile Pro Ala Ile Leu		
170 175 180		
ctg ctg att ggt gtc ttc ctg cca gac agc cca cgt tgg ttt gcc	629	
Leu Leu Ile Gly Val Phe Phe Leu Pro Asp Ser Pro Arg Trp Phe Ala		
185 190 195		
gcc aaa cgc cgt ttt gtt gat gcc gaa cgc gtg ctg cta cgc ctg cgt	677	
Ala Lys Arg Arg Phe Val Asp Ala Glu Arg Val Leu Leu Arg Leu Arg		
200 205 210 215		

gac acc agc gcg gaa gcg aaa cgc gaa ctg gat gaa atc cgt gaa agt		725
Asp Thr Ser Ala Glu Ala Lys Arg Glu Leu Asp Glu Ile Arg Glu Ser		
220	225	230
ttg cag gtt aaa cag agt ggc tgg gcg ctg ttt aaa gag aac agc aac		773
Leu Gln Val Lys Gln Ser Gly Trp Ala Leu Phe Lys Glu Asn Ser Asn		
235	240	245
ttc cgc cgc gcg gtg ttc ctt ggc gta ctg ttg cag gta atg cag caa		821
Phe Arg Arg Ala Val Phe Leu Gly Val Leu Leu Gln Val Met Gln Gln		
250	255	260
ttc acc ggg atg aac gtc atc atg tat tac gcg ccg aaa atc ttc gaa		869
Phe Thr Gly Met Asn Val Ile Met Tyr Tyr Ala Pro Lys Ile Phe Glu		
265	270	275
ctg gcg ggt tat acc aac act acc gag caa atg tgg ggg acc gtg att		917
Leu Ala Gly Tyr Thr Asn Thr Glu Gln Met Trp Gly Thr Val Ile		
280	285	290
295		
gtc ggc ctg acc aac gta ctt gcc acc ttt atc gca atc ggc ctt gtt		965
Val Gly Leu Thr Asn Val Leu Ala Thr Phe Ile Ala Ile Gly Leu Val		
300	305	310
gac cgc tgg gga cgt aaa cca acg cta acg ctg ggc ttc ctg gtg atg		1013
Asp Arg Trp Gly Arg Lys Pro Thr Leu Thr Leu Gly Phe Leu Val Met		
315	320	325
gct gct ggc atg ggc gta ctc ggt aca atg atg cat atc ggt att cac		1061
Ala Ala Gly Met Gly Val Leu Gly Thr Met Met His Ile Gly Ile His		
330	335	340
tct ccg tcg gcg cag tat ttc gcc atc gcc atg ctg ctg atg ttt att		1109
Ser Pro Ser Ala Gln Tyr Phe Ala Ile Ala Met Leu Leu Met Phe Ile		
345	350	355
gtc ggt ttt gcc atg agt gcc ggt ccg ctg att tgg gta ctg tgc tcc		1157
Val Gly Phe Ala Met Ser Ala Gly Pro Leu Ile Trp Val Leu Cys Ser		
360	365	370
375		
gaa att cag ccg ctg aaa ggc cgc gat ttt ggc atc acc tgc tcc act		1205
Glu Ile Gln Pro Leu Lys Gly Arg Asp Phe Gly Ile Thr Cys Ser Thr		
380	385	390
gcc acc aac tgg att gcc aac atg atc gtt ggc gca acg ttc ctg acc		1253
Ala Thr Asn Trp Ile Ala Asn Met Ile Val Gly Ala Thr Phe Leu Thr		
395	400	405
atg ctc aac acg ctg ggt aac gcc aac acc ttc tgg gtg tat gcg gct		1301
Met Leu Asn Thr Leu Gly Asn Ala Asn Thr Phe Trp Val Tyr Ala Ala		
410	415	420
ctg aac gta ctg ttt atc ctg ctg aca ttg tgg ctg gta ccg gaa acc		1349
Leu Asn Val Leu Phe Ile Leu Leu Thr Leu Trp Leu Val Pro Glu Thr		
425	430	435
aaa cac gtt tcg ctg gaa cat att gaa cgt aat ctg atg aaa ggt cgt		1397
Lys His Val Ser Leu Glu His Ile Glu Arg Asn Leu Met Lys Gly Arg		
440	445	450
455		
aaa ctg cgc gaa ata ggc gct cac gat taa tctcccaag cttccccc		1446
Lys Leu Arg Glu Ile Gly Ala His Asp		
460		

<210> 4

<211> 464

<212> PRT

<213> Escherichia coli

<400> 4

Met Pro Asp Ala Lys Lys Gln Gly Arg Ser Asn Lys Ala Met Thr Phe
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Phe Val Cys Phe Leu Ala Ala Leu Ala Gly Leu Leu Phe Gly Leu Asp
20 25 30

Ile Gly Val Ile Ala Gly Ala Leu Pro Phe Ile Ala Asp Glu Phe Gln
35 40 45

Ile Thr Ser His Thr Gln Glu Trp Val Val Ser Ser Met Met Phe Gly
50 55 60

Ala Ala Val Gly Ala Val Gly Ser Gly Trp Leu Ser Phe Lys Leu Gly
65 70 75 80

Arg Lys Lys Ser Leu Met Ile Gly Ala Ile Leu Phe Val Ala Gly Ser
85 90 95

Leu Phe Ser Ala Ala Ala Pro Asn Val Glu Val Leu Ile Leu Ser Arg
100 105 110

Val Leu Leu Gly Leu Ala Val Gly Val Ala Ser Tyr Thr Ala Pro Leu
115 120 125

Tyr Leu Ser Glu Ile Ala Pro Glu Lys Ile Arg Gly Ser Met Ile Ser
130 135 140

Met Tyr Gln Leu Met Ile Thr Ile Gly Ile Leu Gly Ala Tyr Leu Ser
145 150 155 160

Asp Thr Ala Phe Ser Tyr Thr Gly Ala Trp Arg Trp Met Leu Gly Val
165 170 175

Ile Ile Ile Pro Ala Ile Leu Leu Ile Gly Val Phe Phe Leu Pro
180 185 190

Asp Ser Pro Arg Trp Phe Ala Ala Lys Arg Arg Phe Val Asp Ala Glu
195 200 205

Arg Val Leu Leu Arg Leu Arg Asp Thr Ser Ala Glu Ala Lys Arg Glu
210 215 220

Leu Asp Glu Ile Arg Glu Ser Leu Gln Val Lys Gln Ser Gly Trp Ala
225 230 235 240

Leu Phe Lys Glu Asn Ser Asn Phe Arg Arg Ala Val Phe Leu Gly Val
245 250 255

Leu Leu Gln Val Met Gln Gln Phe Thr Gly Met Asn Val Ile Met Tyr
260 265 270

Tyr Ala Pro Lys Ile Phe Glu Leu Ala Gly Tyr Thr Asn Thr Thr Glu
275 280 285

Gln Met Trp Gly Thr Val Ile Val Gly Leu Thr Asn Val Leu Ala Thr
290 295 300

Phe Ile Ala Ile Gly Leu Val Asp Arg Trp Gly Arg Lys Pro Thr Leu
305 310 315 320

Thr Leu Gly Phe Leu Val Met Ala Ala Gly Met Gly Val Leu Gly Thr
325 330 335

Met Met His Ile Gly Ile His Ser Pro Ser Ala Gln Tyr Phe Ala Ile
340 345 350

Ala Met Leu Leu Met Phe Ile Val Gly Phe Ala Met Ser Ala Gly Pro
355 360 365

Leu Ile Trp Val Leu Cys Ser Glu Ile Gln Pro Leu Lys Gly Arg Asp
370 375 380

Phe Gly Ile Thr Cys Ser Thr Ala Thr Asn Trp Ile Ala Asn Met Ile
385 390 395 400

Val Gly Ala Thr Phe Leu Thr Met Leu Asn Thr Leu Gly Asn Ala Asn
405 410 415

Thr Phe Trp Val Tyr Ala Ala Leu Asn Val Leu Phe Ile Leu Leu Thr
420 425 430

Leu Trp Leu Val Pro Glu Thr Lys His Val Ser Leu Glu His Ile Glu
435 440 445

Arg Asn Leu Met Lys Gly Arg Lys Leu Arg Glu Ile Gly Ala His Asp
450 455 460